Biotechnology & Biotechnological Equipment

ISSN: 1310-2818 (Print) 1314-3530 (Online) Journal homepage: http://www.tandfonline.com/loi/tbeq20

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To cite this article: Oeke Yunita, Ike Dhiah Rochmawati, Nur Aini Fadhilah & Njoto Benarkah (2016): Molecular study of intraspecific differences among Sauropus androgynus (L.) Merr. from Indonesia revealed by ITS region variability, Biotechnology & Biotechnological Equipment

To link to this article: http://dx.doi.org/10.1080/13102818.2016.1224978

Published online: 09 Sep 2016.

BIOTECHNOLOGY & BIOTECHNOLOGICAL EQUIPMENT, 2016
http://dx.doi.org/10.1080/13102818.2016.1224978

Taylor & Francis
Taylor & Francis Group

ARTICLE; PHARMACEUTICAL BIOTECHNOLOGY

OPEN ACCESS

Molecular study of intraspecific differences among *Sauropus androgynus* (L.) Merr. from Indonesia revealed by ITS region variability

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ABSTRACT

DNA sequence analysis of the nuclear ribosomal internal transcribed spacer (ITS) region was exploited for its applications in the authentication of *Sauropus androgynus* (L.) Merr. as raw-material herbal medicine and supplement. Leaf samples from 12 different geographic locations in Indonesia were collected. Twelve DNA sequences from the samples were analysed. The sequences were trimmed before sequence alignment. The sequences ranged from 626 to 664 bp in length after trimming. Based on the multiple sequence alignment, a phylogenetic tree was generated using the MrBayes program. It consisted of two groups: one group comprised sequences from Trawas and the other one comprised sequences from Batu, Trawas and Surabaya. These results strongly suggest that ITS sequence analysis is a valuable tool for distinguishing intraspecific differences among *S. androgynus* cultivars from Indonesia.

ARTICLE HISTORY
Received 10 November 2015
Accepted 12 August 2016

KEYWORDS
Internal transcribed spacer; *Sauropus androgynus*; molecular study; sequencing